

University of Groningen

A transnational collaborative network dedicated to the study and applications of the vascular endothelial growth factor-A in medical practice

Stathopoulou, Maria G.; Xie, Ting; Ruggiero, Daniela; Chatelin, Jerome; Rancier, Marc; Weryha, George; Kurth, Mary Jo; Arguinano, Alex-Ander Aldasoro; Gorenjak, Vesna; Petrelis, Alexandros M.

Published in:

Clinical chemistry and laboratory medicine

DOI:

[10.1515/cclm-2017-0838](https://doi.org/10.1515/cclm-2017-0838)

IMPORTANT NOTE: You are advised to consult the publisher's version (publisher's PDF) if you wish to cite from it. Please check the document version below.

Document Version

Publisher's PDF, also known as Version of record

Publication date:

2018

[Link to publication in University of Groningen/UMCG research database](#)

Citation for published version (APA):

Stathopoulou, M. G., Xie, T., Ruggiero, D., Chatelin, J., Rancier, M., Weryha, G., Kurth, M. J., Arguinano, A.-A. A., Gorenjak, V., Petrelis, A. M., Dagher, G., Dedoussis, G., Deloukas, P., Lamont, J., Marc, J., Simmaco, M., van Schaik, R. H. N., Innocenti, F., Merlin, J.-L., ... VEGF Consortium (2018). A transnational collaborative network dedicated to the study and applications of the vascular endothelial growth factor-A in medical practice: the VEGF Consortium. *Clinical chemistry and laboratory medicine*, 56(4), E83-E86. <https://doi.org/10.1515/cclm-2017-0838>

Copyright

Other than for strictly personal use, it is not permitted to download or to forward/distribute the text or part of it without the consent of the author(s) and/or copyright holder(s), unless the work is under an open content license (like Creative Commons).

The publication may also be distributed here under the terms of Article 25fa of the Dutch Copyright Act, indicated by the "Taverne" license. More information can be found on the University of Groningen website: <https://www.rug.nl/library/open-access/self-archiving-pure/taverne-amendment>.

Take-down policy

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

Letter to the Editor

Maria G. Stathopoulou, Ting Xie, Daniela Ruggiero, Jerome Chatelin, Marc Rancier, George Weryha, Mary Jo Kurth, Alex-Ander Aldasoro Arguinano, Vesna Gorenjak, Alexandros M. Petrelis, Georges Dagher, George Dedoussis, Panagiotis Deloukas, John Lamont, Janja Marc, Maurizio Simmaco, Ron H.N. van Schaik, Federico Innocenti, Jean-Louis Merlin, Jochen Schneider, Behrooz Ziad Alizadeh, Marina Ciullo, Sudha Seshadri and Sophie Visvikis-Siest*, The VEGF Consortium

A transnational collaborative network dedicated to the study and applications of the vascular endothelial growth factor-A in medical practice: the VEGF Consortium

<https://doi.org/10.1515/cclm-2017-0838>

Received September 18, 2017; accepted September 19, 2017; previously published online October 31, 2017

Keywords: collaborative network; multidisciplinary genomic studies; personalized medicine; VEGF-A.

To the Editor,

The Vascular Endothelial Growth Factor European Genomic Federation (VEGF) Consortium (www.vegfconsortium.org) was founded in June 2014 by Sophie Visvikis-Siest (chair of the consortium) and an international group of researchers with an interest focused on VEGF-A and its implications in personalized medicine.

Here, we present the VEGF Consortium and describe its objectives and ambitions, its structure and its components together with the methodologies used in projects and preliminary results.

***Corresponding author: Dr. Sophie Visvikis-Siest**, UMR INSERM U1122; IGE-PCV “Gene-Environment Interactions in Cardio-Vascular Physiopathology”, University of Lorraine, 30 Rue Lionnois, 54000 Nancy, France, Phone: +33 (0)6 07 60 25 69, Fax: +33 (0)3 83 32 13 22, E-mail: sophie.visvikis-siest@inserm.fr

Maria G. Stathopoulou, Ting Xie, Jerome Chatelin, Marc Rancier, George Weryha, Alex-Ander Aldasoro Arguinano, Vesna Gorenjak and Alexandros M. Petrelis: UMR INSERM U1122; IGE-PCV “Gene-Environment Interactions in Cardio-Vascular Physiopathology”, University of Lorraine, Nancy, France

Daniela Ruggiero: Institute of Genetics and Biophysics, National Research Council of Italy, Naples, Italy

Mary Jo Kurth and John Lamont: Randox Laboratories Ltd., Crumlin, UK

Georges Dagher: Biobanking and Biomolecular Resources Research Infrastructure (BBMRI)/INSERM US 13, BIOBANQUES, Paris, France

George Dedoussis: Department of Nutrition Dietetics, Harokopio University of Athens, Athens, Greece

Panagiotis Deloukas: Queen Mary University of London, London, UK

The VEGF Consortium aims to develop a transnational collaborative network dedicated to large integrative and multidisciplinary genomic studies of the VEGF-A in order to generate applicable knowledge for medical practice thanks to the following specific objectives:

- to combine data from multiple cohorts in order to identify VEGF-A ‘-omics’ profiling in health and non-communicable diseases
- to elucidate the pivotal role of VEGF-A in the pathophysiology of non-communicable diseases
- to demonstrate the patients’ stratification potential of VEGF-A ‘-omics’ profiling
- to implement the research results into clinical practice and establish the role of VEGF-A as a predictive, preventive, diagnostic and prognostic biomarker
- to provide information on the effect of VEGF-A ‘-omics’ profiling in side effects and response to therapy through pharmacogenomics studies

Janja Marc: Faculty of Pharmacy, University of Ljubljana, Ljubljana, Slovenia

Maurizio Simmaco: Sant’Andrea Hospital – Sapienza University of Rome, Rome, Italy

Ron H.N. van Schaik: European Society of Pharmacogenomics and Personalised Therapy (ESPT), Nancy, France

Federico Innocenti: University of North Carolina at Chapel Hill, Chapel Hill, NC, USA

Jean-Louis Merlin: Institut de Cancérologie de Lorraine et Université de Lorraine, Vandoeuvre les Nancy, France

Jochen Schneider: University of Luxembourg, Luxembourg, Europe
Behrooz Ziad Alizadeh: Department of Epidemiology, University of Groningen, University Medical Center Groningen, Groningen, The Netherlands

Marina Ciullo: Institute of Genetics and Biophysics, National Research Council of Italy, Naples, Italy; and IRCCS Neuromed, Pozzilli, Isernia, Italy

Sudha Seshadri: Department of Neurology, Boston University School of Medicine, Boston, MA, USA

- to propose implementation strategies and European guidelines involving VEGF-A ‘-omics’ profiling for the management of non-communicable diseases
- to share methodologies, data and knowledge in the field of ‘-omics’ management and innovative statistics
- to develop standardized teaching and evaluation methods practiced and validated by the consortium.

It comprises 11 working groups, where the partners of the consortium are participating based on their expertise:

1. VEGF-A ‘-omics’ profiling in health
2. VEGF-A ‘-omics’ profiling in diseases
3. ‘-Omics’ technologies
4. Methodological aspects
5. VEGF-A clinical implementation
6. Pharmagenomics
7. Endothelins and endothelial factors
8. VEGF-A basic research (cancer cell lines, animal models)
9. VEGF-A and inflammation
10. Communication and scientific/educational meetings
11. Raising awareness of populations

Prospective, longitudinal, family-based or population-based cohorts of healthy individuals are the core of the consortium. These are the following:

1. The STANISLAS family study: This is a longitudinal family structure cohort of community-based population of French origin recruited in 1993–1995, followed up for 15 years. A number of 1006 nuclear families comprising two parents and at least two biological children over 6 years old are included in the study [1].
2. The Framingham Heart Study: It is an ongoing, longitudinal, community-based, observational cohort study that was initiated in 1948 to prospectively investigate the risk factors for cardiovascular disease (CVD). The original cohort enrolled 5209 men and women, the offspring cohort enrolled 5124 participants (including 3514 biological offspring) and Gen 3 included 4095 individuals [2–4].
3. Cilento study: This is a population-based study that aims at identifying genetic risk factors for common diseases and traits. The sample includes isolated populations from three villages (Campora, Gioi and Cardile). The overall sample size of individuals participating to the study is 2100 [5].
4. The LifeLines Cohort Study and Biobank (LLs): LLs is a multidisciplinary prospective population-based cohort study examining the health and health-related behaviors of 167,000 persons living in the north east

region of The Netherlands in a three-generation design [6].

Furthermore, cohorts of patients and case-control studies are also included in the consortium:

5. The Hellenic Study of Interactions between SNPs and Eating in Atherosclerosis Susceptibility: case-control study of coronary artery disease.
6. Ljubljana patients: case-control studies recruited from Ljubljana, Slovenia that include cases of osteoporosis, osteoarthritis, CVD and diabetes [7–9].

In addition, partners of the consortium have access to large biobanks such as the UK Biobank (Panagiotis Deloukas), Biobanking and Biomolecular Resources Research Infrastructure – European Research Infrastructure Consortium BBMRI-ERIC (including Sophie Visvikis-Siest with the Biological Resources Center IGE-PCV – BB-0033-00051) and the Alliance for Clinical Trials in Oncology (Federico Innocenti).

Given the wide range of the research field and the need for application of different methodologies in order to successfully achieve its objectives, the consortium is composed of scientists with different and complementary expertise and with a large range of resources such as large study populations, research materials and harmonized data.

Although the VEGF Consortium was officially founded on 2014, it was based on the long-term collaboration between some of its founding partners. Therefore, a number of significant results have been published already, and many projects are ongoing, with promising preliminary results.

Among the most basic steps was the identification through two genome-wide association studies (GWAS) of 10 genetic variants that explain >50% of the circulating VEGF-A levels variability [10, 11]. This is a unique finding among GWAS. In most GWAS, the identified variants do not explain >10% of the individual variability of the assessed traits. This finding has strengthened our belief that VEGF-A will indeed be used as strong biomarker for personalized medicine. Significant associations between some of these polymorphisms and intermediate phenotypes of chronic diseases have been identified since then: high-density and low-density lipoprotein [12], L-selectin gene expression [13] and free tri-iodothyronine (FT3) levels [14]. Significant epistatic interactions between these variants were observed for intercellular adhesion molecule 1 (ICAM-1), E-selectin, interleukin 6 and tumor necrosis factor α (TNF- α) plasma levels [13]. Concerning specific disease risk, we have shown

that these polymorphisms and/or their epistatic interactions can affect the risk for depression [15], and for autoimmune thyroid diseases [14], whereas no associations were found for diabetes type 2 [16].

Concerning the expression isoforms of *VEGF-A* gene, we have shown that these are significantly associated with ICAM-1, L-selectin and TNF- α expression [13] and with specific autoimmune thyroid diseases [17].

Furthermore, we have also identified associations between VEGF-A circulating levels and thyroid hormones levels [17] and with ICAM-1 and E-selectin levels [13].

Through a candidate gene approach of polymorphisms in genes involved in angiogenesis, we have identified direct and epistatic effects of variants on nitric oxide synthase 3 (*NOS3*), *CD14*⁺ monocytes, matrix metalloproteinases (*MMPs*) and interleukin 4 receptor (*ILR4*) genes with levels of VEGF-A and VEGF-A expression isoforms, but also gene \times environment interactions [18].

An important result is also the production of two patents based on the results of studies performed by partners of the consortium [19, 20].

Several projects are ongoing and focused on CVD intermediate phenotypes, thyroid diseases, cancer and stroke.

Three face-to-face meetings have been organized to date: Paris (2014), Budapest (2015) and Santorini (2016).

The VEGF Consortium is an ambitious international collaboration that aims to pave the way for the implementation of VEGF-A in personalized medicine and routine clinical practice. The designed projects take advantage of the wide expertise of its partners, the large infrastructures of cohorts and biobanks and a combination of the most up-to-date “-omics” approaches for generating multidimensional data, as well as ‘systems medicine’ approaches, network analysis and computational modeling methodologies.

Among its major originalities is that it integrates commercialization and communication platforms, targeting the valid and easy measurement of the identified biomarkers in large-scale settings but also the education of the general population, patients, scientists and health practitioners.

The VEGF Consortium is a novel consortium with an innovating structure and original goals. The ultimate goal is to ameliorate life expectancy, quality of life for individuals and financial benefits for health systems.

Author contributions: All the authors have accepted responsibility for the entire content of this submitted manuscript and approved submission.

Research funding: None declared.

Employment or leadership: None declared.

Honorarium: None declared.

Competing interests: The funding organization(s) played no role in the study design; in the collection, analysis, and interpretation of data; in the writing of the report; or in the decision to submit the report for publication.

References

1. Visvikis-Siest S, Siest G. The STANISLAS Cohort: a 10-year follow-up of supposed healthy families. Gene-environment interactions, reference values and evaluation of biomarkers in prevention of cardiovascular diseases. *Clin Chem Lab Med* 2008;46:733–47.
2. Splansky GL, Corey D, Yang Q, Atwood LD, Cupples LA, Benjamin EJ, et al. The Third Generation Cohort of the National Heart, Lung, and Blood Institute's Framingham Heart Study: design, recruitment, and initial examination. *Am J Epidemiol* 2007;165:1328–35.
3. Dawber T, Meadors G, Moore F. Epidemiological approaches to heart disease: the Framingham Study. *Am J Public Health Nations Health* 1951;41:279–81.
4. Feinleib M, Kannel W, Garrison R, McNamara P, Castelli W. The Framingham Offspring Study. Design and preliminary data. *Prev Med* 1975;4:518–25.
5. Colonna V, Nutile T, Ferrucci RR, Fardella G, Aversano M, Barbuiani G, et al. Comparing population structure as inferred from genealogical versus genetic information. *Eur J Hum Genet* 2009;17:1635–41.
6. Scholtens S, Smidt N, Swertz MA, Bakker SJ, Dotinga A, Vonk JM, et al. Cohort profile: LifeLines, a three-generation cohort study and biobank. *Int J Epidemiol* 2015;44:1172–80.
7. Estrada K, Styrkarsdottir U, Evangelou E, Hsu YH, Duncan EL, Ntzani EE, et al. Genome-wide meta-analysis identifies 56 bone mineral density loci and reveals 14 loci associated with risk of fracture. *Nat Genet* 2012;44:491–501.
8. Mirjanic-Azaric B, Vekic J, Zeljkovic A, Jelic-Ivanovic Z, Djerić M, Milivojac T, et al. Interrelated cathepsin S-lowering and LDL subclass profile improvements induced by atorvastatin in the plasma of stable angina patients. *J Atheroscler Thromb* 2014;21:868–77.
9. Zupan J, van't Hof RJ, Vindisar F, Haring G, Trebse R, Komadina R, et al. Osteoarthritic versus osteoporotic bone and intra-skeletal variations in normal bone: evaluation with microCT and bone histomorphometry. *J Orthop Res* 2013;31:1059–66.
10. Choi SH, Ruggiero D, Sorice R, Song C, Nutile T, Vernon Smith A, et al. Six novel loci associated with circulating VEGF levels identified by a meta-analysis of genome-wide association studies. *PLoS Genet* 2016;12:e1005874.
11. Debette S, Visvikis-Siest S, Chen MH, Ndiaye NC, Song C, Destefano A, et al. Identification of cis- and trans-acting genetic variants explaining up to half the variation in circulating vascular endothelial growth factor levels. *Circ Res* 2011;109:554–63.
12. Stathopoulou MG, Bonnefond A, Ndiaye NC, Azimi-Nezhad M, El Shamieh S, Saleh A, et al. A common variant highly associated

- with plasma VEGFA levels also contributes to the variation of both LDL-C and HDL-C. *J Lipid Res* 2012;54:535–41.
13. Azimi-Nezhad M, Stathopoulou MG, Bonnefond A, Rancier M, Saleh A, Lamont J, et al. Associations of vascular endothelial growth factor (VEGF) with adhesion and inflammation molecules in a healthy population. *Cytokine* 2013;61:602–7.
 14. Zaaber I, Rancier M, Stathopoulou MG, Saleh A, Marmouch H, Masson C, et al. Plasma VEGF-related polymorphisms are implied in autoimmune thyroid diseases. *Autoimmunity* 2016;49:229–35.
 15. Xie T, Stathopoulou MG, de Andres F, Siest G, Murray H, Martin M, et al. VEGF-related polymorphisms identified by GWAS and risk for major depression. *Transl Psychiatry* 2017;7:e1055.
 16. Bonnefond A, Saulnier PJ, Stathopoulou MG, Grarup N, Ndiaye NC, Roussel R, et al. What is the contribution of two genetic variants regulating VEGF levels to type 2 diabetes risk and to microvascular complications? *PLoS One* 2013;8:e55921.
 17. Rancier M, Zaaber I, Stathopoulou MG, Chatelin J, Saleh A, Marmouch H, et al. Pro- and anti-angiogenic VEGF mRNAs in autoimmune thyroid diseases. *Autoimmunity* 2016;49:366–72.
 18. Saleh A, Stathopoulou MG, Dade S, Ndiaye NC, Azimi-Nezhad M, Murray H, et al. Angiogenesis related genes NOS3, CD14, MMP3 and IL4R are associated to VEGF gene expression and circulating levels in healthy adults. *BMC Med Genet* 2015;16:90.
 19. Visvikis-Siest S. Association of vascular endothelial growth factor genetic variant with metabolic syndrome, 2014. Patent number: WO2014006231 A1. Available at: <http://www.google.com.pg/patents/WO2014006231A1?cl=en&hl=fr>. Accessed: 1 June 2017.
 20. Randox. Identification of genetic variants – VEGF, 2012. Patent number: US20130202587 A1. Available at: <https://www.google.com/patents/US20130202587>. Accessed: 1 June 2017.